

Slebodyn
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#22

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/830,111D

DATE: 07/15/2003

TIME: 14:08:26

Input Set : N:\CrF4\07092003\I830111D.raw

Output Set: N:\CRF4\07152003\I830111D.raw

1 <110> APPLICANT: Kaneka Corporation
 2 Matsuda, Hideyuki
 3 Kawamukai, Makota
 4 Yajima, Kazuyoshi
 5 Ikenaka, Yasuhiro
 6 Hasegawa, Junzo
 7 Takahashi, Satomi
 8 <120> TITLE OF INVENTION: Process For Producing Coenzyme Q10
 9 <130> FILE REFERENCE: 21581-00265-US
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/830,111D
 11 <141> CURRENT FILING DATE: 2001-07-23
 12 <160> NUMBER OF SEQ ID NOS: 2
 13 <170> SOFTWARE: PatentIn version 3.2
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 1653
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Saioella complicata
 19 <400> SEQUENCE: 1

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22	aaatccatat accatggcct caccagact gcggatacga agcatcagct ctgcgtcaat	180
23	cgcctctcg cgatcggtta ccctaagaac agcctcgca ctttcattac gactaagatg	240
24	taccccgacg agccggccat cgagttcatg ggctgtctgt gtgtcttcgg cgtcgagact	300
25	ggtttagccct gatccgaatc aacctctcat caatccgctc aacttggctg gtcccggat	360
26	gtcaaatttt acatccaaca tccgatctct cctcggttca ggacaccctt ctctcgacac	420
27	tgtcgctaaa tactatgttc agtctgaggg aaagcatatt cgtccgctca tggtaactgct	480
28	gatggctcag gcgacggagg ttgcgc当地 agttcagggt tgggagaagg tcgtggaggt	540
29	tccggtaac gagggactcg caccaccaga ggtgctcaat gacaagaacc cagatatgat	600
30	gaacatgagg tcaggaccat taacgaagga cggcgagatc gagggacaga cgtcgaat	660
31	cctcgctcg caacggcggt tgctgagat cacggagatg atccatgcag catcactcct	720
32	ccacgacgac gttatcgacg ctcccgagac cagacaaac gcaccatcc gaaaccaggc	780
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36	gacgcaggaa acgttcgatt actatttgcga gaagacttac ttgaagactg cgtccttgc	1020
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39	ctacaccgtc tccgctaccg acctcggtaa gcccgccggt gcagacctcc agctcggtct	1200
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45      ggcatgcaag cttggctgtt ttggcgatg agagaagatt ttcagcctga tacagattaa 1560
46      atcagaacgc agaagcggtc tgataaaaaca gaatttgcct ggcggcagta gcgcgggtgg 1620
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50 <211> LENGTH: 440
51 <212> TYPE: PRT
52 <213> ORGANISM: Saitoella complicata
53 <400> SEQUENCE: 2
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57          20          25          30
58      Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser Ser Trp Ala Ala
59          35          40          45
60      Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp Pro Asn Gln Pro
61          50          55          60
62      Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu Met Ser Asn Leu Thr
63          65          70          75          80
64      Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly His Pro Ser Leu Asp Thr
65          85          90          95
66      Val Ala Lys Tyr Tyr Val Gln Ser Glu Gly Lys His Ile Arg Pro Leu
67          100         105         110
68      Met Val Leu Leu Met Ala Gln Ala Thr Glu Val Ala Pro Lys Val Gln
69          115         120         125
70      Gly Trp Glu Lys Val Val Glu Val Pro Val Asn Glu Gly Leu Ala Pro
71          130         135         140
72      Pro Glu Val Leu Asn Asp Lys Asn Pro Asp Met Met Asn Met Arg Ser
73          145         150         155         160
74      Gly Pro Leu Thr Lys Asp Gly Glu Ile Glu Gly Gln Thr Ser Asn Ile
75          165         170         175
76      Leu Ala Ser Gln Arg Arg Leu Ala Glu Ile Thr Glu Met Ile His Ala
77          180         185         190
78      Ala Ser Leu Leu His Asp Asp Val Ile Asp Ala Ser Glu Thr Arg Arg
79          195         200         205
80      Asn Ala Pro Ser Gly Asn Gln Ala Phe Gly Asn Lys Met Ala Ile Leu
81          210         215         220
82      Ala Gly Asp Phe Leu Leu Gly Arg Ala Ser Val Ala Leu Ala Arg Leu
83          225         230         235         240
84      Arg Asn Pro Glu Val Ile Glu Leu Leu Ala Thr Val Ile Ala Asn Leu
85          245         250         255
86      Val Glu | Gly Glu Phe Met Gln Leu Lys Asn Thr Val Asp Asp Ala Ile
87          260         265         270
88      Glu Ala Thr Ala Thr Gln Glu Thr Phe Asp Tyr Tyr Leu Gln Lys Thr
89          275         280         285
90      Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys Arg Ala Ser Ala
91          290         295         300
92      Leu Leu Gly Gly Ala Thr Pro Glu Val Ala Asp Ala Ala Tyr Ala Tyr
93          305         310         315         320
94      Gly Arg Asn Leu Gly Leu Ala Phe Gln Ile Val Asp Asp Met Leu Asp

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96	Tyr Thr Val Ser Ala Thr Asp Leu Gly Lys Pro Ala Gly Ala Asp Leu		
97	340	345	350
98	Gln Leu Gly Leu Ala Thr Ala Pro Ala Leu Phe Ala Trp Lys His His		
99	355	360	365
100	Ala Glu Leu Gly Pro Met Ile Lys Arg Lys Phe Ser Asp Pro Gly Asp		
101	370	375	380
102	Val Glu Arg Ala Arg Glu Leu Val Glu Lys Ser Asp Gly Leu Glu Lys		
103	385	390	395
104	400	405	410
105	Thr Arg Ala Leu Ala Glu Glu Tyr Ala Gln Lys Ala Leu Asp Ala Ile		
106	415	420	425
107	Arg Thr Phe Pro Glu Ser Pro Ala Arg Lys Ala Leu Glu Gln Leu Thr		
108	430	435	440
109	Asp Lys Val Leu Thr Arg Ser Arg		

VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Wrong Format